

SEQUENCE PROTOCOL

5 <110> Degussa AG
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 15 <170> PatentIn Ver. 2.1
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 <212> DNA
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 caggcataac ccctaaaata ccctgatctt cccccgtgct ctgccccctg gtccaccctt 240
 35 gcgtacataa taggacgc atg gga aaa cat gag gtt gct cag cag acg gtt 291
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 1 5 10
 40 ccg ggt cct tgc ccg gaa atg gaa gcg cag cgg cgt aaa gag ttg cgc 339
 Pro Gly Pro Ser Pro Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg
 15 20 25
 45 aag cac aag gcc att gcc act ggc ctg ttg att ttt gct gcc gct gta 387
 Lys His Lys Ala Ile Ala Thr Gly Leu Leu Ile Phe Ala Ala Val
 30 35 40
 50 tat ttt ctt tgc cgt ttc gtg gag acc cgt ccg ggt gaa act gca gcg 435
 Tyr Phe Leu Cys Arg Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala
 45 50 55
 tgg gta ggt ttt gtg cgc gct gcg gca gag gcc gga atg att ggc ggg 483
 Trp Val Gly Phe Val Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly
 60 65 70 75
 55 ttg gcc gac tgg ttc gcg gtc acc gcg ctg ttc cgt cat cca ttg tgg 531
 Leu Ala Asp Trp Phe Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp
 80 85 90

	ctg cct att ccg cac act gcg att atc ccg cgc aag aaa gac cag tta	579
	Leu Pro Ile Pro His Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu	
	95 100 105	
5	ggg gag gcc tta agc ggg ttt gtg ggg gat aac ttc cta aat gcc cag	627
	Gly Glu Ala Leu Ser Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln	
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10	ctc att acg gaa aaa gtc tct cag gcg cgg atc cca gag cgc gcc ggg	675
	Leu Ile Thr Glu Lys Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly	
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15	gag tgg ctc gcc cag ccg gaa aac ggg gag aaa gtt tcg cgc gaa gtc	723
	Glu Trp Leu Ala Gln Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val	
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20	ggc aaa ttg acc gct aat att gtg cgc gca atc gat ccg tca gat gct	771
	Gly Lys Leu Thr Ala Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala	
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25	gaa cgc gtg att aaa tct gcg gtg atc gac aag ctt gcg gaa ccc acc	819
	Glu Ala Val Ile Lys Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr	
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30	tgg ggc cca cca gct ggg cgg ttg ctg gaa caa ctc ctc gcc gaa gca	867
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35	aag ccg aac cag ttg tcc agg aac tcg cgc agt ggc tgc aca aaa agg	915
	Lys Pro Asn Gln Leu Ser Arg Asn Ser Arg Ser Gly Cys Thr Lys Arg	
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40	cgt tgg gct ccc gag ccg ctg att gat cgc ctg ctc aac gag cgc cgc	963
	Arg Trp Ala Pro Glu Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg	
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45	ccg att tgg gcg ccg aaa ttc act gcg cag ctg gtc agc ggc aaa gtc	1011
	Pro Ile Trp Ala Pro Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val	
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50	tat gac gag gtc ata aaa ttc act gaa gcc gtc gct gcc gat cct aac	1059
	Tyr Asp Glu Val Ile Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn	
	255 260 265	
55	cac gag gcc cgc aaa tcg ctg cgc cga ttc ctt aat aaa ttg gcg caa	1107
	His Glu Ala Arg Lys Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln	
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60	gac ctg cag cat gac cca ggc atg att att aaa gtt gaa gaa atc aaa	1155
	Asp Leu Gln His Asp Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys	
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65	gcg gac atc atg ggc tcc ggc gcc atc gcg caa gcc gcg cca acc atc	1203
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	Trp Ala Ser Ala Ser Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser	
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 Ser Ile Leu Arg Arg Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln
 335 340 345

5

aga ttg ctt gtc gac gac tcc ctc cgg cat tca ctc gac acc cgg att 1347
 Arg Leu Leu Val Asp Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile
 350 355 360

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acc ggc gcc gct gct ttc ctc gcc gac aat tac gcc ccc gaa gtc acc 1395
 Thr Gly Ala Ala Ala Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr
 365 370 375

15

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 Gly Ile Ile Ser Glu Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser
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20

gag aaa atc gaa ctc atg gtg ggc aaa gac ctc caa tac atc cgc ctt 1491
 Glu Lys Ile Glu Leu Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu
 400 405 410

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aat ggc aca att gta ggt gca tta gca gga ctg gcc att tac gct att 1539
 Asn Gly Thr Ile Val Gly Ala Leu Ala Glu Leu Ala Ile Tyr Ala Ile
 415 420 425

tcc cat atc ctc ttc gga gct taactaggag taaccatcat gtccgatgca 1590
 Ser His Ile Leu Phe Gly Ala
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aaagacgatt ccattctgtc caagtggagc aatgcagctt ccgagctcag cggtgccgtc 1650
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 <213> Corynebacterium glutamicum

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Ala Thr Gly Leu Leu Ile Phe Ala Ala Ala Val Tyr Phe Leu Cys Arg
 35 40 45

55

Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val
 50 55 60
 Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe
 65 70 75 80

Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp Leu Pro Ile Pro His
85 90 95

5 Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser
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Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys
115 120 125

10 Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln
130 135 140

Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala
145 150 155 160

15 Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys
165 170 175

20 Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala
180 185 190

Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Ala Lys Pro Asn Gln Leu
195 200 205

25 Ser Arg Asn Ser Arg Ser Gly Cys Thr Lys Arg Arg Trp Ala Pro Glu
210 215 220

Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro
225 230 235 240

30 Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile
245 250 255

Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys
260 265 270

35 Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp
275 280 285

40 Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly
290 295 300

Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser
305 310 315 320

45 Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg
325 330 335

Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp
340 345 350

50 Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala
355 360 365

55 Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu
370 375 380

Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu
385 390 395 400

Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val
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5 Gly Ala Leu Ala Gly Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe
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